

FIG.1

1 CCTTCATACC GGCCCTTCCC CTCGGCTTTG CCTGGACAGC TCCTGCCTCC CGCAGGGCCC
 61 ACCTGTGTCC CCCAGCGCCG CTCCACCCAG CAGGCCTGAG CCCCTCTCTG CTGCCAGACA
 121 CCCCTGCTG CCCACTCTCC TGCTGCTCGG GTTCTGAGGC ACAGCTTGTC ACACCGAGGC
 181 GGATTCTCTT TCTCTTTCTC TTCTGGCCCA CAGCCGCAGC AATGGCGCTG AGTTCCTCTG
 241 CTGGAGTTCA TCCTGCTAGC TGGGTTCCCG AGCTGCCGGT CTGAGCCTGA GGCATGGAGC
 M E

 301 CTCCTGGAGA CTGGGGGCCT CCTCCCTGGA GATCCACCCC CAGAACCGAC GTCTTGAGGC
 P P G D W G P P P W R S T P R T D V L R

 361 TGGTGCTGTA TCTCACCTTC CTGGGAGCCC CCTGCTACGC CCCAGCTCTG CCGTCCTGCA
 L V L Y L T F L G A P C Y A P A L P S C

 421 AGGAGGACGA GTACCCAGTG GGCTCCGAGT GCTGCCCCAA GTGCAGTCCA GGTTATCGTG
 K E D E Y P V G S E C C P K C S P G Y R

 481 TGAAGGAGGC CTGCGGGGAG CTGACGGGCA CAGTGTGTGA ACCCTGCCCT CCAGGCACCT
 V K E A C G E L T G T V C E P C P P G T

 541 ACATTGCCCA CCTCAATGGC CTAAGCAAGT GTCTGCAGTG CCAAATGTGT GACCCAGCCA
 Y I A H L N G L S K C L Q C Q M C D P A

 601 TGGGCCTGCG CGCGAGCCGG AACTGCTCCA GGACAGAGAA CGCCGTGTGT GGCTGCAGCC
 M G L R A S R N C S R T E N A V C G C S

 661 CAGGCCACTT CTGCATCGTC CAGGACGGGG ACCACTGCGC CGCGTGCCGC GCTTACGCCA
 P G H F C I V Q D G D H C A A C R A Y A

 721 CCTCCAGCCC GGGCCAGAGG GTGCAGAAGG GAGGCACCGA GAGTCAGGAC ACCCTGTGTC
 T S S P G Q R V Q K G G T E S Q D T L C

 781 AGAACTGCCC CCCGGGGACC TTCTCTCCCA ATGGGACCCT GGAGGAATGT CAGCACCAGA
 Q N C P P G T F S P N G I L E E C Q H Q

 841 CCAAGTGCAG CTGGCTGGTG ACGAAGGCCG GAGCTGGGAC CAGCAGCTCC CACTGGGTAT
 T K C S W L V T K A G A G T S S S H W V

 901 GGTGGTTTCT CTCAGGGAGC CTCGTATCG TCATTGTTTG CTCCACAGTT GGCCTAATCA
 W W F L S G S L V I V I V C S T V G L I

FIG.2A

961 TATGTGTGAA AAGAAGAAAG CCAAGGGGTG ATGTAGTCAA GGTGATCGTC TCCGTCCAGC
 I C V K R R K P R G D V V K V I V S V Q
 1021 GGAAAAGACA GGAGGCAGAA GGTGAGGCCA CAGTCATTGA GGCCCTGCAG GCCCCTCCGG
 R K R Q E A E G E A T V I E A L Q A P P
 1081 ACGTCACCAC GGTGGCCGTG GAGGAGACAA TACCCTCATT CACGGGGAGG AGCCCAAACC
 D V T T V A V E E T I P S F T G R S P N
 1141 ACTGACCCAC AGACTCTGCA CCCCAGCGCC AGAGATACCT GGAGCGACGG CTGCTGAAAG
 H -
 1201 AGGCTGTCCA CCTGGCGAAA CCACCGGAGC CCGGAGGCTT GGGGGCTCCG CCCTGGGCTG
 1261 GCTTCCGTCT CCTCCAGTGG AGGGAGAGGT GGGGCCCTG CTGGGGTAGA GCTGGGGACG
 1321 CCACGTGCCA TTCCCATGGG CCAGTGAGGG CCTGGGGCCT CTGTTCTGCT GTGGCCTGAG
 1381 CTCCCCAGAG TCCTGAGGAG GAGCGCCAGT TGCCCCTCGC TCACAGACCA CACACCCAGC
 1441 CCTCCTGGGC CAGCCCAGAG GGCCCTTCAG ACCCCAGCTG TCTGCGCGTC TGACTCTTGT
 1501 GGCCTCAGCA GGACAGGCC CGGGCACTGC CTCACAGCCA AGGCTGGACT GGGTTGGCTG
 1561 CAGTGTGGTG TTTAGTGGAT ACCACATCGG AAGTGATTTT CTAAATTGGA TTTGAATTCC
 1621 GGTCTGTCT TCTATTTGTC ATGAAACAGT GTATTTGGGG AGATGCTGTG GGAGGATGTA
 1681 AATATCTTGT TTCTCCTCAA AAAAAAAAAA AAAAAAAAAA AAAA

FIG.2B

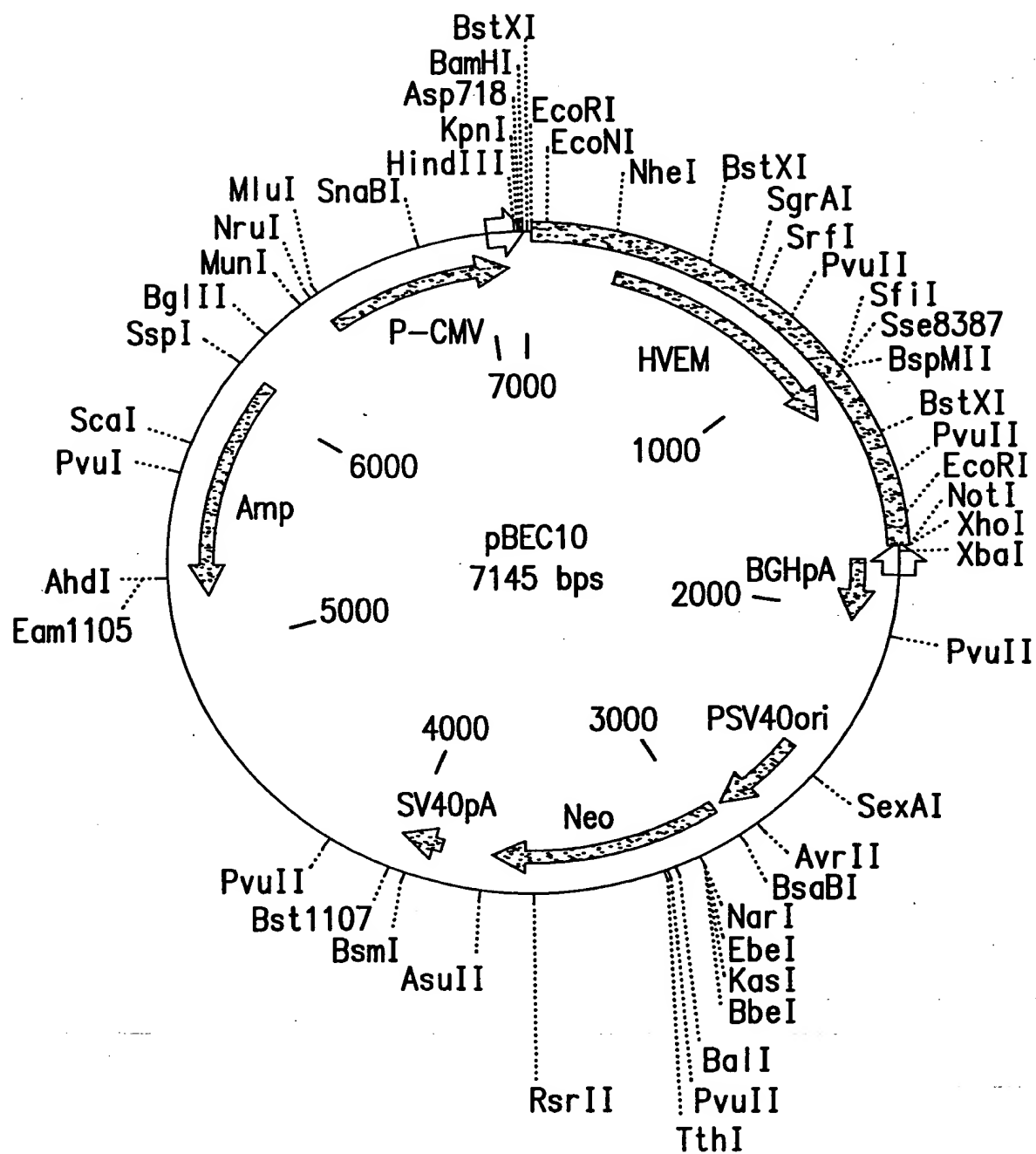


FIG.3

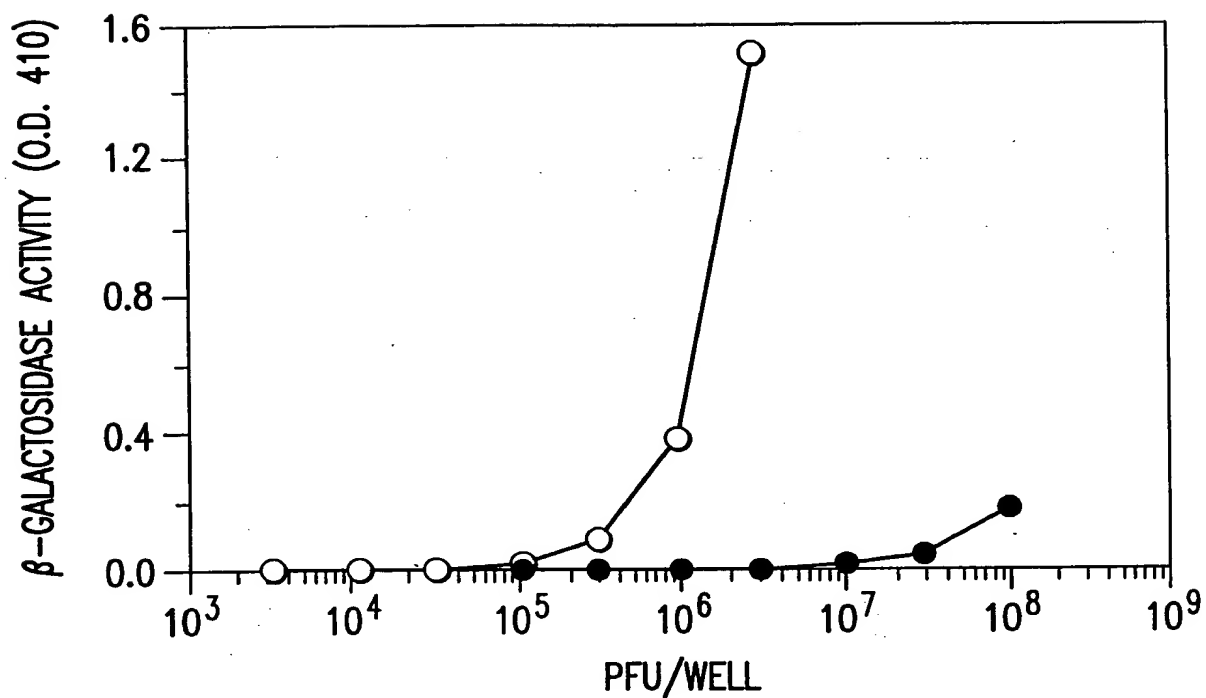


FIG. 4A

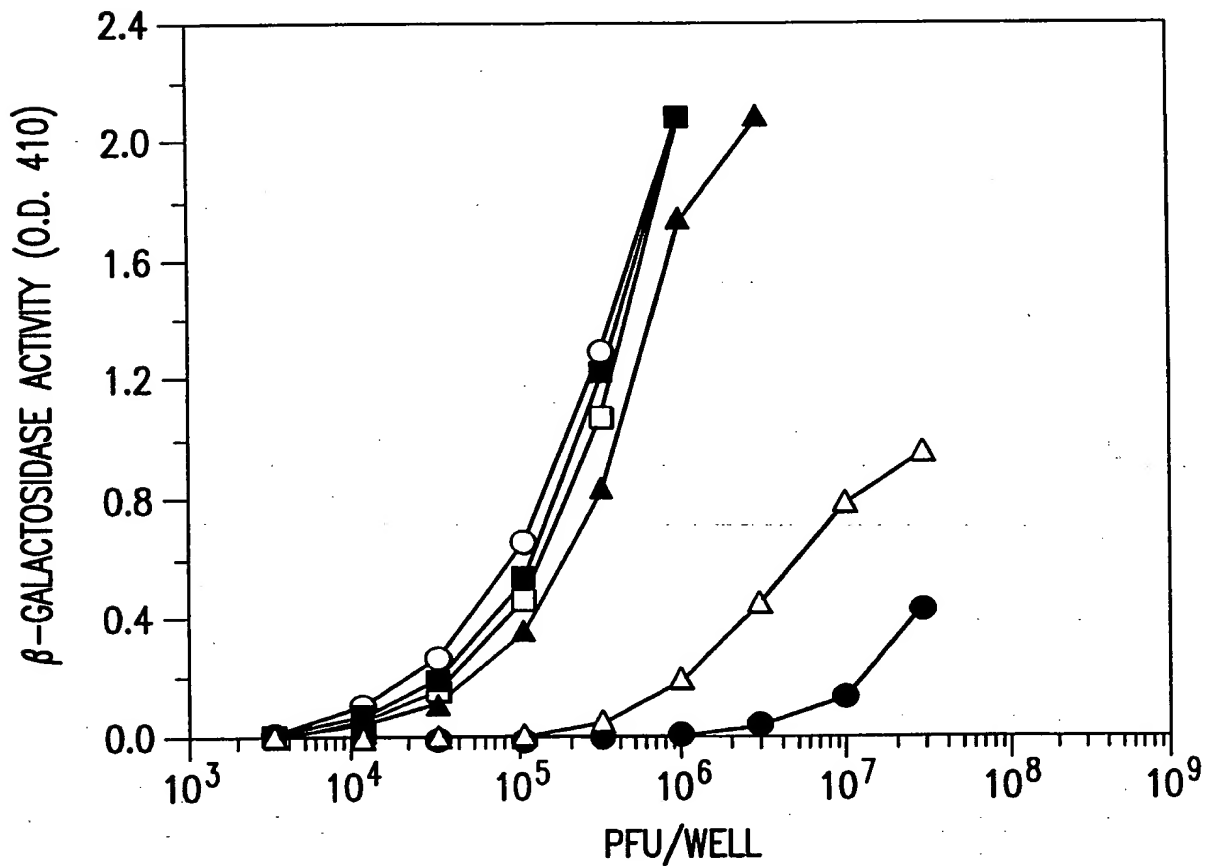


FIG. 4B

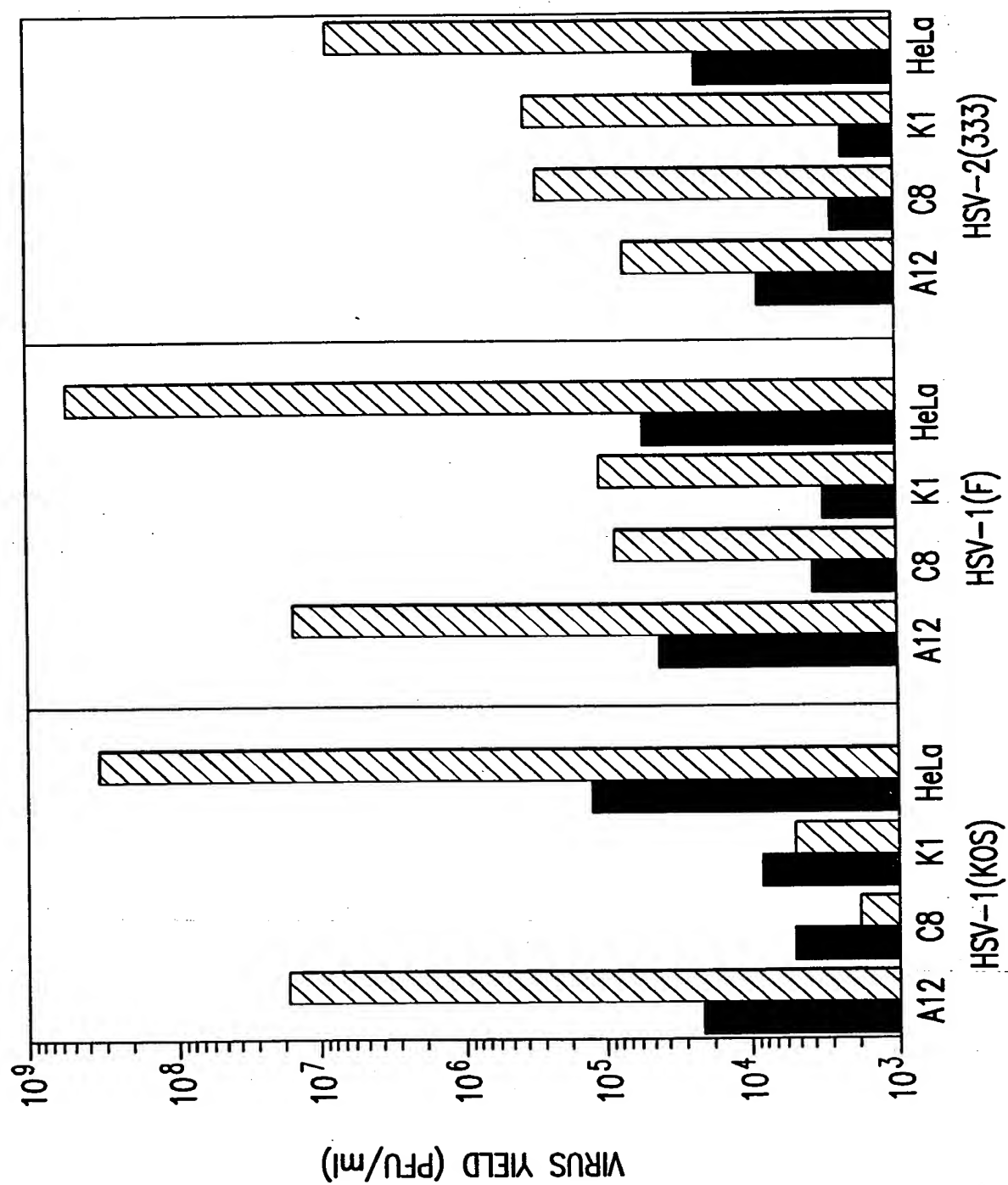


FIG. 5

gD-1 AND gD-2 INTERFERE WITH KOS(gL86) INFECTION OF A12 CELLS

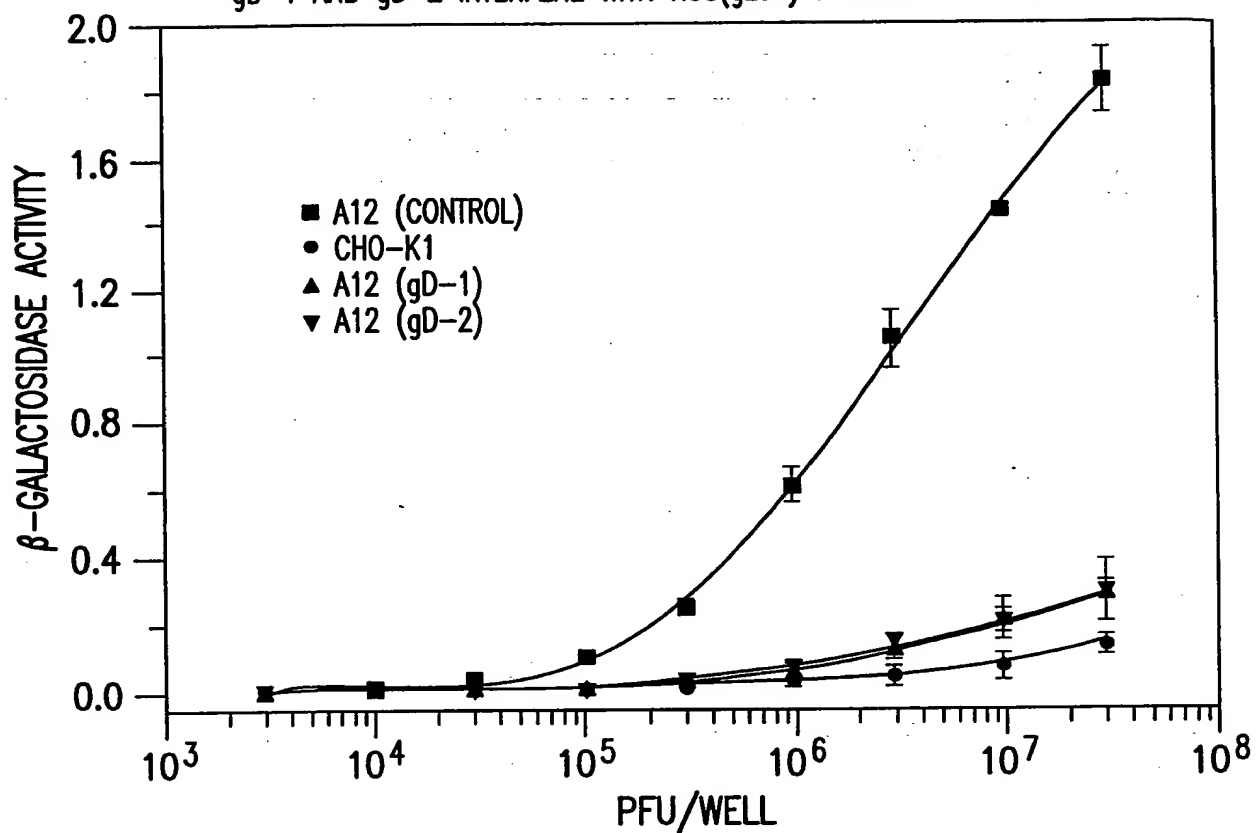


FIG. 6A

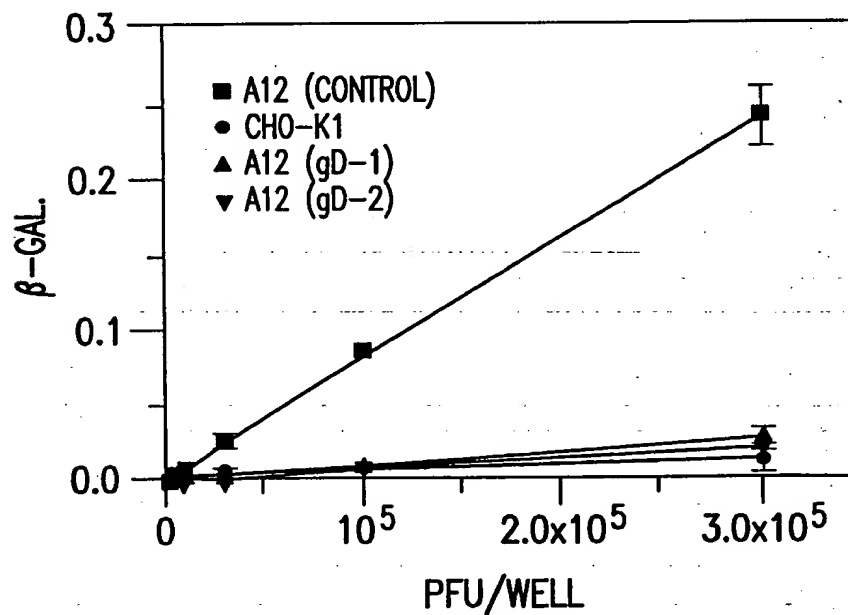


FIG. 6B

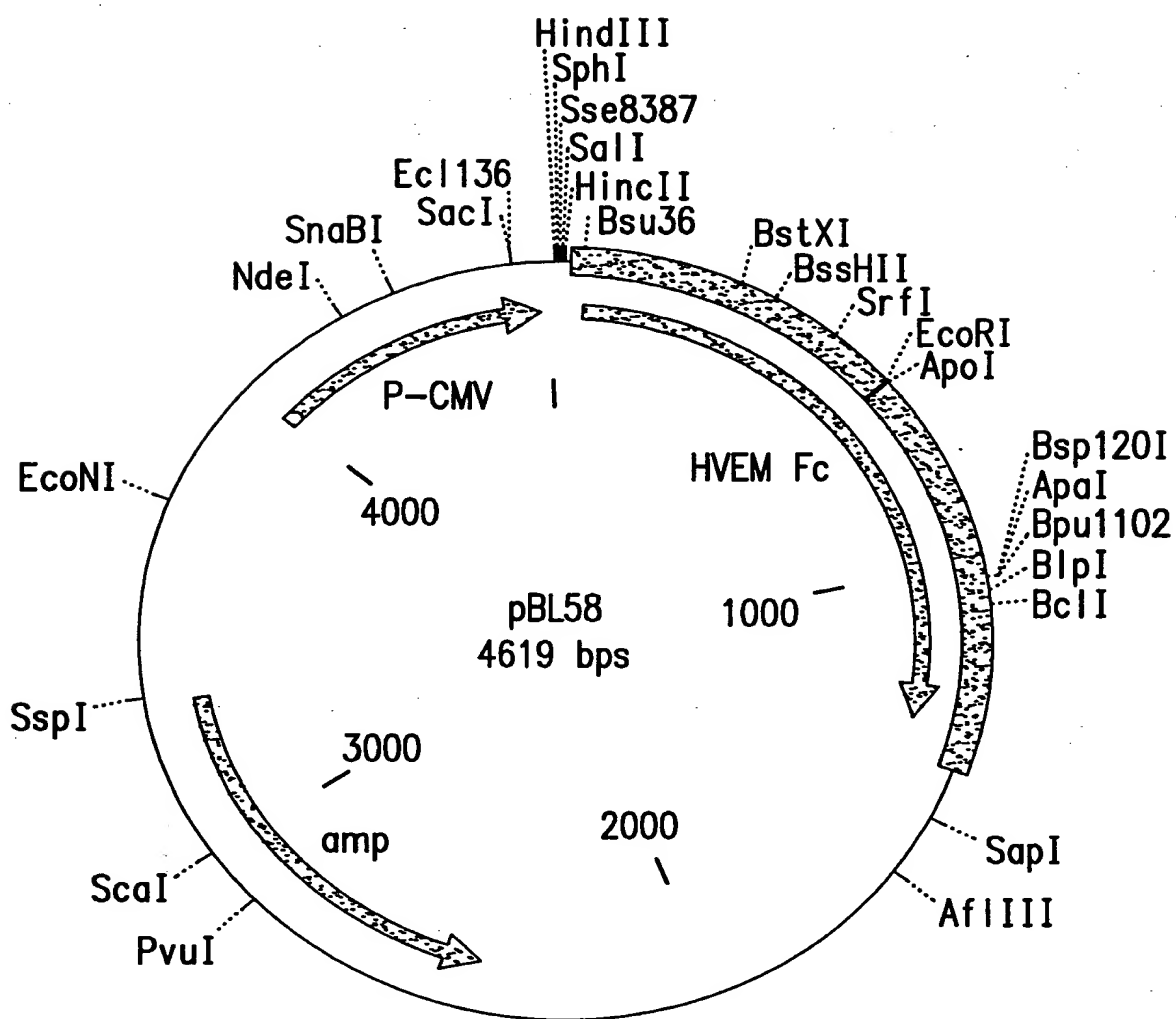


FIG.7

1 AAGCTTGCAT GCCTGCAGGT CGACTCTAGC TGGGTTCCCG AGCTGCCGGT CTGAGCCTGA
 61 GGCATGGAGC CTCCTGGAGA CTGGGGGCCT CCTCCCTGGA GATCCACCCC CAGAACCGAC
 M E P P G D W G P P P W R S T P R T D

 121 GTCTTGAGGC TGGTGCTGTA TCTCACCTTC CTGGGAGCCC CCTGCTACGC CCCAGCTCTG
 V L R L V L Y L T F L G A P C Y A P A L

 181 CCGTCCTGCA AGGAGGACGA GTACCCAGTG GGCTCCGAGT GCTGCCCCAA GTGCAGTCCA
 P S C K E D E Y P V G S E C C P K C S P

 241 GGTTATCGTG TGAAGGAGGC CTGCGGGGAG CTGACGGGCA CAGTGTGTGA ACCCTGCCCT
 G Y R V K E A C G E L T G T V C E P C P

 301 CCAGGCACCT ACATTGCCCA CCTCAATGGC CTAAGCAAGT GTCTGCAGTG CCAAATGTGT
 P G T Y I A H L N G L S K C L Q C Q M C

 361 GACCCAGCCA TGGGCCTGCG CGCGAGCCGG AACTGCTCCA GGACAGAGAA CGCCGTGTGT
 D P A M G L R A S R N C S R T E N A V C

 421 GGCTGCAGCC CAGGCCACTT CTGCATCGTC CAGGACGGGG ACCACTGCGC CGCGTGCCGC
 G C S P G H F C I V Q D G D H C A A C R

 481 GCTTACGCCA CCTCCAGCCC GGGCCAGAGG GTGCAGAAGG GAGGCACCGA GAGTCAGGAC
 A Y A T S S P G Q R V Q K G G T E S Q D

 541 ACCCTGTGTC AGAACTGCCC CCCGGGGACC TTCTCTCCA ATGGGACCCT GGAGGAATGT
 T L C Q N C P P G T F S P N G I L E E C

 601 CAGCACCAGA CCAAGTGCAG AATTCACAAG ACCGTTGCAC CCTCGACATG CAGCAAGCCC
 Q H Q T K C R I H K T V A P S T C S K P

 661 ACGTGCCAC CCCCTGAACT CCTGGGGGGA CCGTCTGTCT TCATCTTCCC CCCAAAACCC
 T C P P P E L L G G P S V F I F P P K P

 721 AAGGACACCC TCATGATCTC ACGCACCCCC GAGGTCACAT GCGTGGTGGT GGACGTGAGC
 K D T L M I S R T P E V T C V V V D V S

 781 CAGGATGACC CCGAGGTGCA GTTCACATGG TACATAAACA ACGAGCAGGT GCGCACCGCC
 Q D D P E V Q F T W Y I N N E Q V R T A

FIG.8A

841 CGGCCGCCGC TACGGGAGCA GCAGTTCAAC AGCACGATCC GCGTGGTCAG CACCCTCCCC
R P P L R E Q Q F N S T I R V V S T L P

901 ATCACGCACC AGGACTGGCT GAGGGCAAG GAGTTCAAGT GCAAAGTCCA CAACAAGGCA
I T H Q D W L R G K E F K C K V H N K A

961 CTCCCGGCCC CCATCGAGAA AACCATCTCC AAAGCCAGAG GGCAGCCCCT GGAGCCGAAG
L P A P I E K T I S K A R G Q P L E P K

1021 GTCTACACCA TGGGCCCTCC CCGGGAGGAG CTGAGCAGCA GGTGCGTCAG CCTGACCTGC
V Y T M G P P R E E L S S R S V S L T C

1081 ATGATCAACG GCTTCTACCC TTCCGACATC TCGGTGGAGT GGGAGAAGAA CGGGAAGGCA
M I N G F Y P S D I S V E W E K N G K A

1141 GAGGACAACT ACAAGACCAC GCCGGCCGTG CTGGACAGCG ACGGCTCCTA CTCCTCTAC
E D N Y K T T P A V L D S D G S Y F L Y

1201 AACAAAGCTCT CAGTGCCAC GAGTGAGTGG CAGCGGGGCG ACGTCTTCAC CTGCTCCGTG
N K L S V P T S E W Q R G D V F T C S V

1261 ATGCACGAGG CTTGCACAA CCACTACACG CAGAAGTCCA TCTCCCGCTC TCCGGGTAAA
M H E A L H N H Y T Q K S I S R S P G K

1321 TGAGCGCTGT GCCGGCGAGC TGCCCCTCTC CCTCCCCCCC ACGCCGCAGC TGTGCACCCC
1381 GCACACAAAT AAAGCACCCA GCTCTGCCCT GAACAGCTTC CGGTCTCCCT ATAGTGAGTC
1441 GTATTAATTT CGATAAGCCA GCTGCATTAA TGAATCGGCC AACGCGCGGG GAGAGGCGGT
1501 TTGCGTATTG GGCCTCTTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC GGTCGTTTCGG
1561 CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGGTAATAC GGTTATCCAC AGAATCAGGG
1621 GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG
1681 GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAAATCGA
1741 CGCTCAAGTC AGAGGTGGCG AAACCCGACA GGAATAATAA GATACCAGGC GTTTCCCCCT
1801 GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC
1861 TTTCTCCCTT CGGGAAGCGT GGCGCTTTCT CATAGCTCAC GCTGTAGGTA TCTCAGTTCG
1921 GTGTAGGTCG TTCGCTCAA GCTGGGCTGT GTGCACGAAC CCCCCGTTCA GCCCGACCGC
1981 TGCCTTTAT CCGGTAACCTA TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA
2041 CTGGCAGCAG CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG
2101 TTCTTGAAGT GGTGGCCTAA CTACGGCTAC ACTAGAAGGA CAGTATTTGG TATCTGCGCT
2161 CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC
2221 ACCGCTGGTA GCGGTGGTTT TTTTGGTTTG AAGCAGCAGA TTACGCGCAG AAAAAAAGGA

FIG.8B

2281 TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAAACTCA
 2341 CGTTAAGGGA TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT
 2401 TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT AAACCTGGTC TGACAGTTAC
 2461 CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTTCGTC ATCCATAGTT
 2521 GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT
 2581 GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG
 2641 CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT
 2701 ATTAATTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT
 2761 GTTGCCATTG CTACAGGCAT CGTGGTGTC ACGCTCGTCG TTGGTATGGC TTCATTGAGC
 2821 TCCGGTTCCC AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA AAAAGCGGTT
 2881 AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG
 2941 GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG
 3001 ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT
 3061 TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC
 3121 ATTGGAAAAC GTTCTTCGGG GCGAAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT
 3181 TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT
 3241 TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGACACGG
 3301 AAATGTTGAA TACTCATACT CTTCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT
 3361 TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG
 3421 CGCACATTTT CCCGAAAAGT GCCACCTGAC GTCTAAGAAA CCATTATTAT CATGACATTA
 3481 ACCTATAAAA ATAGGCGTAT CACGAGGCC TTTCTGTCTCG CGCGTTTCGG TGATGACGGT
 3541 GAAAACCTCT GACACATGCA GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC
 3601 GGGAGCAGAC AAGCCCGTCA GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCTGGCTT
 3661 AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGACC ATATCGACGC TCTCCCTTAT
 3721 GCGACTCCTG CATTAGGAAG CAGCCCAGTA GTAGGTTGAG GCCGTTGAGC ACCGCCGCCG
 3781 CAAGGAATGG TGCAAGGAGA TGGCGCCCAA CAGTCCCCCG GCCACGGGGC CTGCCACCAT
 3841 ACCCACGCCG AAACAAGCGC TCATGAGCCC GAAGTGCGCA GCCCGATCTT CCCCATCGGT
 3901 GATGTCGGCG ATATAGGCGC CAGCAACCGC ACCTGTGGCG CCGGTGATGC CGGCCACGAT
 3961 GCGTCCGGCG TAGAGGATCT GGCTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT
 4021 CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC GCCTGGCTGA
 4081 CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT AGTAACGCCA
 4141 ATAGGGACTT TCCATTGACG TCAATGGGTG GACTATTTAC GGTAAACTGC CCACTTGGA
 4201 GTACATCAAG TGTATCATAT GCCAAGTACG CCCCTATTG ACGTCAATGA CGGTAAATGG
 4261 CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT TTCCTACTTG GCAGTACATC
 4321 TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT CAATGGGCGT
 4381 GGATAGCGGT TTGACTCAGG GGGATTTCCA AGTCTCCACC CCATTGACGT CAATGGGAGT
 4441 TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAACAACCTC CGCCCCATTG
 4501 ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC TCTCTGGCTA
 4561 ACTAGAGAAC CCACTGCTTA ACTGGCTTAT CGAAATTAAT ACGACTCACT ATAGGGAGAC
 4621 CC

FIG.8C

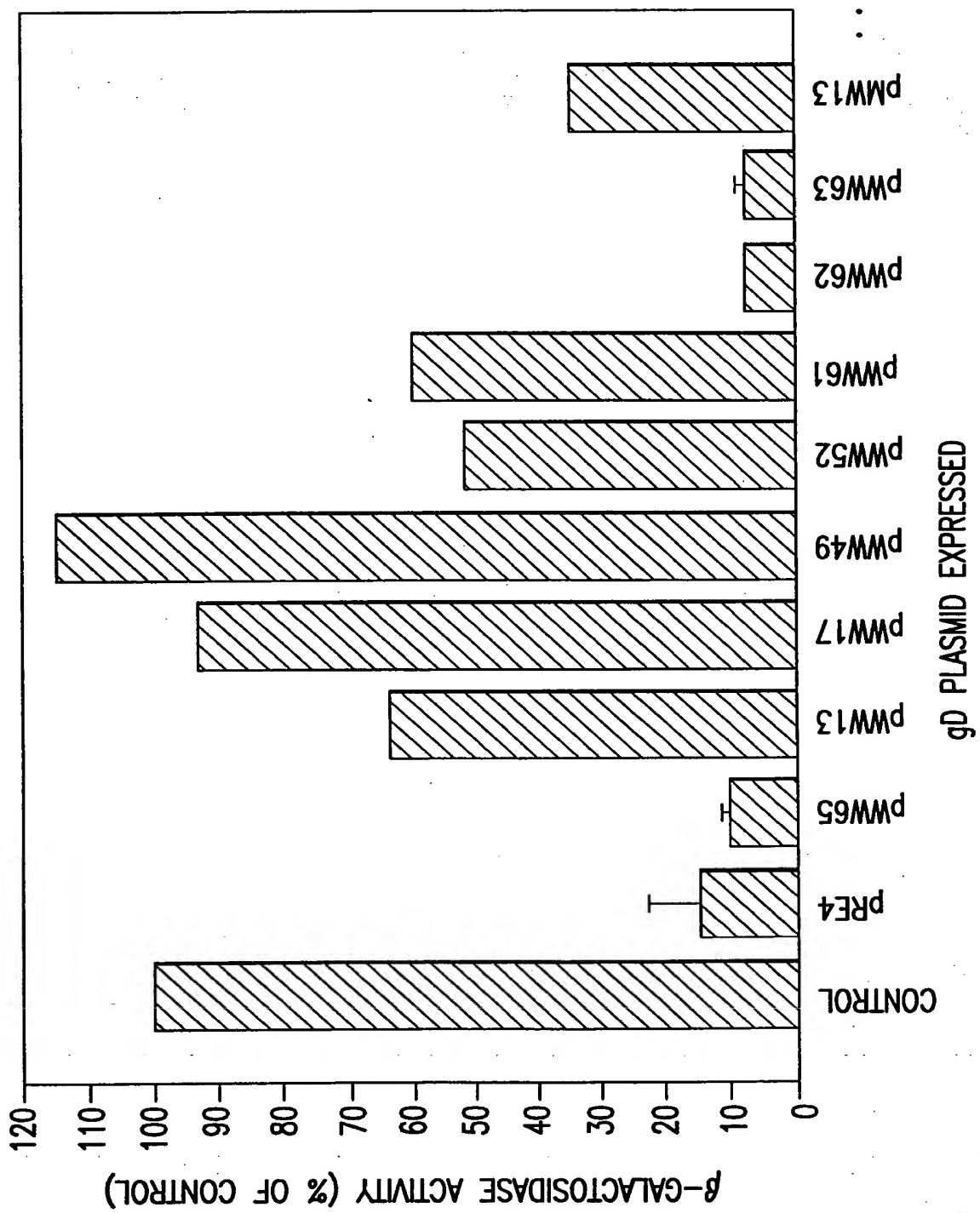


FIG.10